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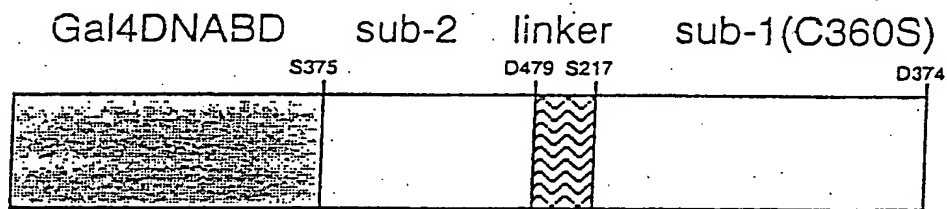


Fig. 1

1/1 CGG CAC GAG GGC CTG GGC AAC GGC CGG CAC ACG CTG GGA CAG CAG GAA GTG GAA GTG GAC
 R H E G L G N G R H T L G Q Q E V E V D
 61/21 GGT CTG ACG GCC TAC GTG GCA GGT GAG CGC CCT GAC CCA CTG GGT CCC AGG TCC CAG CCC
 G L T A Y V A G E R P D P L G P R S Q P
 121/41 GCA TGC CAG GTG GCC CAC GAC CCC CCC AGA GCC TGC CCT CTC TGC TCT CAA GGC ACC AAG
 A C Q V A H D P P R A C P L C S Q G T K
 181/61 ACG CTG AGT GGC AGC ATA GCC CCA ATG AAC GTC TGT GTC CGG GCA CTT CCT GCA GGC CAC
 T L S G S I A P M N V C V R A L P A G H
 241/81 AGG TTC AGC ATG AAG TCG GCC TTG AAG GCT GCA TCC TTG CAC CCC GCC CAG TTG CTG GCG
 R F S M K S A L K A S L H P A Q L L G
 301/101 CTG GAG AAG AGT AAG GGG ACC TTG ACT TTG GTG CTG ACG CAG ACT TCG TGG TGC TCG ACG
 L E K S K G T L T L V L T Q T S W C S T
 361/121 ACT CCC TTC ACG TCC AGG CCA CCT ACA TCT CGG GTG AGC TGG TGT GGC AGG CGG ACC CAG
 T P F T S R P P T S R V S W C G R R T Q
 421/141 CTA GGC AGT GAC AAG GAC CTC GGC TGA
 L G S D K D L G *

Fig. 2

1/1 31/11
 ggc gcg gct ccg ctc tcg gct ggg gtt cgt cac tgg gcg cgg gat ttg gcc gcc gcg ggg
 G A A P L S A G V R H W A R D L A A A G
 61/21 91/31
 ctc egg agc cgc tcg ctc ccg aca cgg ctc acg atg cgc ggc gac agg gcc ggc ggg ggc
 L R S R S L P T R L T M R G D R A G G G
 121/41 151/51
 ccc gtg ctc cag ttc act aac tgc cgg atc ctg cgc gga ggg aaa ctg ctc agg gag gat
 P V L Q F T N C R I L R G G K L L R E D
 181/61 211/71
 ctg tgg gtg cgc gga ggc cgc atc ttg gac cca gag aag ctg ttc ttt gag gag cgg cgc
 L W V R G G R I L D P E K L F F E E R R
 241/81 271/91
 gtg gcc gac gag cgg cgg gac tgc ggg ggc cgc atc ttg gct ccc gga ttc atc gac gtg
 V A D E R R D C G G R I L A P G F I D V
 301/101 331/111
 cag atc aac cgt gga TTT GGT GTT GAC TTC TCT CAA GCC ACG GAG GAC GTG GGT TCG GGG
 Q I N R G F G V D F S Q A T E D V G S G
 361/121 391/131
 GTT GCC CTC GTG GCC CGG AGG ATC CTG TCG CAC GGC GTC ACC TCC TTC TGC CCC ACC CTG
 V A L V A R R I L S H G V T S F C P T L
 421/141 451/151
 GTC ACT TCC CCA CCG GAG GCT TAT CAC AAG GTT GTT CCT CAG ATC CCT GTG AAG AGT GGT
 V T S P P E A Y H K V V P Q I P V K S G
 481/161 511/171
 GGT CCC CAT GGG GCA GGG GTC CTC GGG CTG CAC CTG GAG GGC CCC TTC ATC AGC CGG GAG
 G P H G A G V L G L H L E G P F I S R E
 541/181 571/191
 AAG CGG GGC GCG CAC CCC GAG GCC CAC CTC CGC TCC TTC GAG GCC GAT GCC TTC CAG GAC
 K R G A H P E A H L R S F E A D A F Q D
 601/201 631/211
 TTG CTG GCC ACC TAC GGG CCC CTG GAC AAT GTC CGC ATC GTG ACG CTG GCC CCA GAG TTG
 L L A T Y G P L D N V R I V T L A P E L
 661/221 691/231
 GGC CGT AGC CAC GAA GTG ATC CGG GCG CTG ACG GCC CGT GGC ATC TGC GTG TCC CTA GGG
 G R S H E V I R A L T A R G I C V S L G
 721/241 751/251
 CAC TCA GTG GCT GAC CTG CGG GCG GCA GAG GAT GCT GTG TGG AGC GGA GCC ACC TTC ATC
 H S V A D L R A A E D A V W S G A T F I
 781/261 811/271
 ACC CAC CTC TTC AAC GCC ATG CTG CCT TTC CAC CAC CGC GAC CCA GGC ATC GTG GGG CTC
 T H L F N A M L P F H H R D P G I V G L

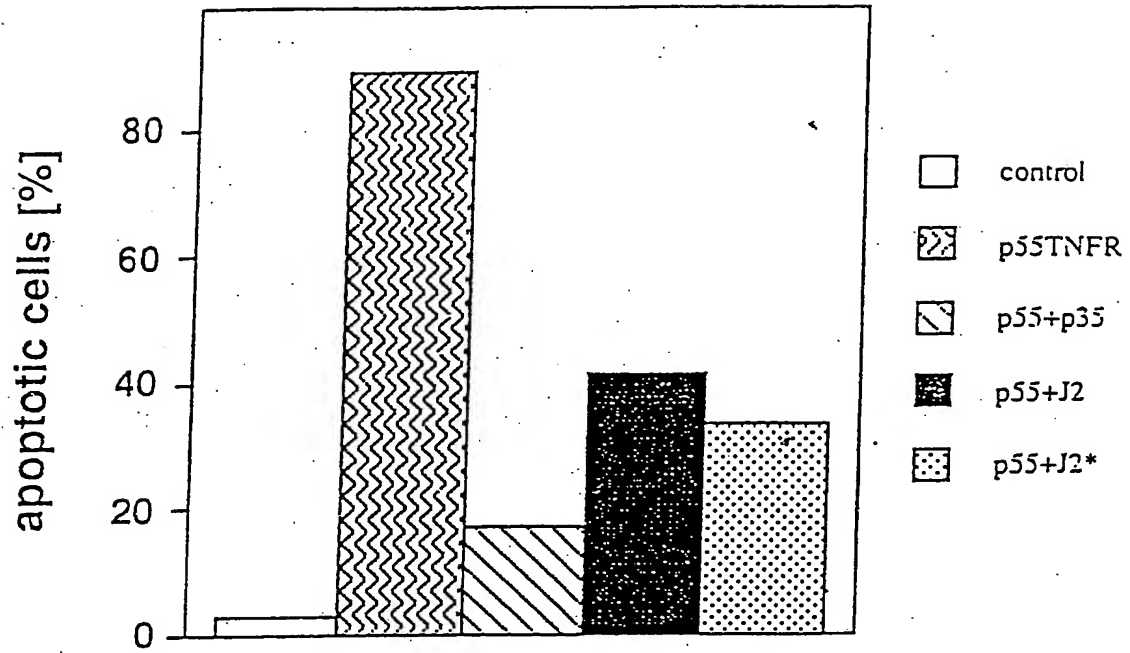
Fig. 3

841/281
 CTG ACC AGC GAC CGG CTG CCC GCA GGC CGC TGC ATC TTC TAT GGG ATG ATT GCA GAT GGC
 L T S D R L P A G R C I F Y G M I A D G
 901/301
 ACG CAC ACC AAC CCC GCC GCC CTG CGG ATC GCC CAC CGT GCC CAT CCC CAG GGG CTG GTG
 T H T N P A A L R I A H R A H P Q G L V
 961/321
 CTG GTC ACC GAT GCC ATC CCT GCC TTG GGC CTG GGC AAC GGC CGG CAC ACG CTG GGA CAG
 L V T D A I P A L G L G N G R H T L G Q
 1021/341
 CAG GAA GTG GAA GTG GAC GGT CTG ACG GCC TAC GTG GCA GGT GAG CGC CCT GAC CCA CTG
 Q E V E V D G L T A Y V A G E R P D P L
 1081/361
 GGT CCC AGG TCC CAG CCC GCA TGC CAG GTG GCC CAC GAC CCC CCC AGA GCC TGC CCT CTC
 G P R S Q P A C Q V A H D P P R A C P L
 1141/381
 TGC TCT CAA GGC ACC AAG ACG CTG AGT GGC AGC ATA GCC CCA ATG AAC GTC TGT GTC CGG
 C S Q G T R T L S G S I A P M N V C V R
 1201/401
 CAC TTC CTG CAG GCC ACA GGC TGC AGC ATG GAG TCG GCC CTG GAG GCT GCA TCC CTG CAC
 H F L Q A T G C S M E S A L E A A S L H
 1261/421
 CCC GCC CAG TTG CTG GGG CTG GAG AAG AGT AAG GGG ACC CTG GAC TTT GGT GCT GAC GCA
 P A Q L L G L E K S K G T L D F G A D A
 1321/441
 GAC TTC GTG GTG CTC GAC GAC TCC CTT CAC GTC CAG GCC ACC TAC ATC TCG GGT GAG CTG
 D F V V L D D S L H V Q A T Y I S G E L
 1381/461
 GTG TGG CAG GCG GAC GCA GGT AGG CAG TGA CAA GGA CCT CGG CTG AGA GGA CAC CTG GCC
 V W Q A D A A R Q
 1441
 GCA GCG GGA TGC CAT CAG GGC CGG GTG GTT GGG GAG CTG GTC TCC AGG GAG TGA GTC GGG
 1501
 AGC CCT GCT GGA T

Fig. 3 (a)

A

HEK 293-T cells



HeLa cells

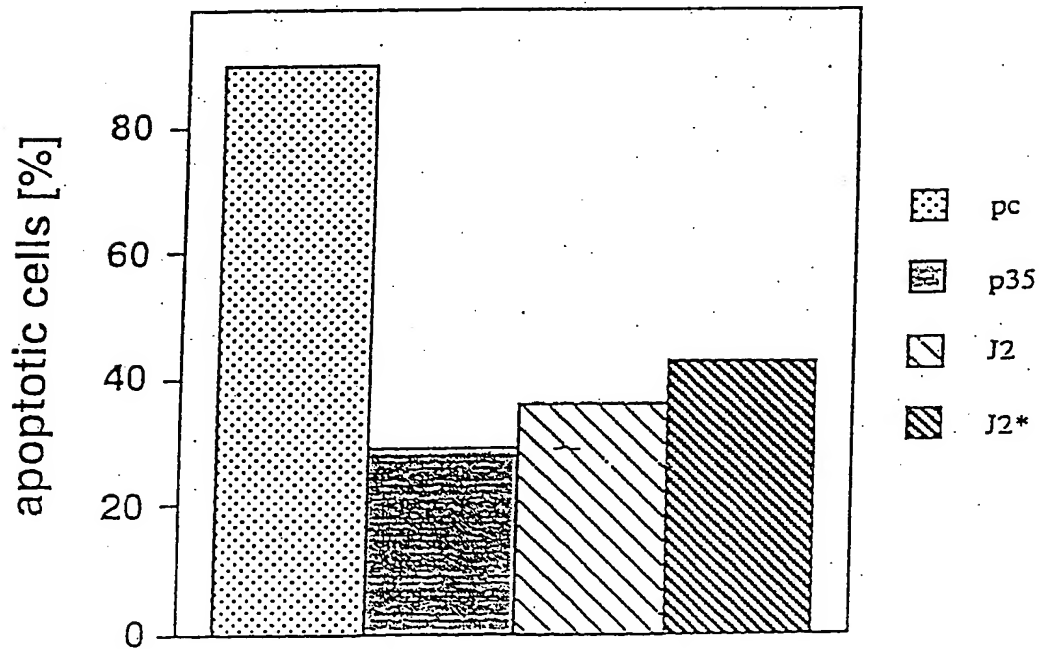


Fig. 4

	1	10	20	30	40	50	60	70	80	90	100
1	GAGCAGCTCA	AAACTACAGT	CCAGGTGATC	AAGAGGTGAG	CCAAGCCGAG	TGAGAAGCCC	CGGCTGCGGC	AGATACCCTC	GGCTGAAGAC	CTGGAGACAG	100
101	ATGGCGGGG	ACCGGGCCAG	GTGGTGGACG	ATGGCCTGGA	GCACAGGGAG	CTGGGCCATG	GGCAGCCTGA	GGCCAGAGGC	CCCGCTCCTC	TCCAGCAGCA	200
201	CCCTCAGGTG	TTGCTCTGGG	AACAGCAGCG	ACTGGCTGGG	CGGCTCCCCC	GGGCAGCAC	CGGGGACACT	GTGCTGCTTC	CTCTGGCCCC	GGGTGGGCAC	300
301	CGGCCCTCTGT	CCCGGGCTCA	GTCTTCCCCA	GCCGCACCTG	CCTCACTGTC	AGCCCCAGAG	CCTGCCAGCC	AGGCCGAGT	CCTCTCCAGC	TCAGAGACCC	400
401	CTGCCAGGAC	CCTGCCCTTC	ACCACAGGGC	TGATCTATGA	CTCGGTCATG	CTGAAGCACC	AGTGCTCCTG	CGGTGACAAC	AGCAGGCACC	CGGAGCACGC	500
501	CGGCCGCATC	CAGAGCATCT	GGTCCCGGCT	GCAGGAGCGG	GGGCTCCGGA	GCCAGTGTGA	GTGTCTCCGA	GGCCGGNAGG	CCTCCCTGGA	AGAGCTGCAG	600
601	TCGGTCCACT	CTGAGCGGCA	CGTGCTCCTC	TACGGCACCA	ACCGGCTCAG	CCGCCTCAAA	CTGGACACAG	GGAAGCTGGC	AGGGCTCCTG	GCACAGCGGA	700
701	TGTTTGTGAT	GCTGCCCTGT	GGTGGGGTTG	GGGTGGACAC	TGACACCATC	TGGATGAGC	TTCATTCTCTC	CAATGCAGCC	CGCTGGGCCG	CTGGCAGTGT	800
801	CACTGACCTC	GCCTTCAAG	TGGCTTCTCG	TGAGCTAAG	AATGGTTTCG	CTGTGGTGCG	GCCCCCAGGA	CACCATGCAG	ATCATTTCAAC	AGCCATGGGC	900
901	TTCTGCTTCT	TCAACTCAGT	GGCCATCGCC	TGCCGGCAGC	TGCAACAGCA	GAGCAAGGCC	AGCAAGATCC	TCATTGTAGA	CTGGGACGTG	CACCATGGCA	1000
1001	ACGGCACCCA	GCAAACCTTC	TACCAAGACC	CCAGTGTGCT	CTACATCTCC	CTGCATCGCC	ATGACGACGG	CAACTTCTTC	CCAGGGAGTG	GGGCTGTGGA	1100
1101	TGAGGTAGGG	GCTGGCAGCG	GTGAGGGCTT	CAATGTCAAT	GTGGCCTGGG	CTGGAGGTCT	GGACCCCCCC	ATGGGGGATC	CTGAGTACCT	GGCTGCTTTC	1200
1201	AGGATAGTCG	TGATGCCCAT	CGCCCGAGAG	TTCTCTCCAG	ACCTAGTCCT	GGTGTCTGCT	GGATTTGATG	CTGCTGAGGG	TCACCCCGCC	CCACTGGGTG	1300
1301	GCTACCATGT	TTCTGCCAAA	TGTTTGGAT	ACATGACGCA	GCAACTGATG	AACCTGGCAG	GAGGCGCAGT	GGTGTGGCC	TTGGAGGGTG	GCCATGACCT	1400
1401	CACAGCCATC	TGTGACGCCCT	CTGAGGCCCTG	TGTGGCTGCT	CTTCTGGGTA	ACAGGGTGGG	TCCCCCTTCA	GAAAGNAGGCT	GGAAACAGNA	ACCCANCTC	1500
1501	AATTCCATCC	GCTCTCTGGA	GGCCCTGATC	CGGGTGCACA	GTAATACTG	GGGCTGCATG	CAGCGCCTGG	CCTCCTGTCC	AGACTCCTCG	GTGCCCTAGAG	1600
1601	TGCCAGGGGC	TGACAAAGAA	GAAGTGGAGG	CAGTAACCGC	ACTGGCGTCC	CTCTCTGTGG	GCATCCTGGC	TGAAGATAGG	CCCTCGGAGC	AGCTGGTGGA	1700
1701	GGAGGAAGAA	CCTATGAATC	TCTAA								1725

Fig. 5A

		10		20		30		40		50		60		70		80		90		100
1	EQKTHVQVI	KRS	AKPSEKP	RLRQIPSAED	LET	DGGGPGQ	VVDDGLEHRE	LGHGQPEAR	G	PAPLQHPQV	LLWEQQR	LAG	RLPRGSTGDT	VLLPLAQCGH	100					
101	RPLSRAQSSP	AAPASLSAPE	PASQARVLSS	SETPARTLPF	TTGLIYDSVM	LKHQCSCGD	NRHPEHAGRI	QSIWSRLQER	GLRSQCECLR	GRKASLEELQ	200									
201	SVHSERHVLL	YGTNPLSRLK	LDNGKLAGLL	AQRMFVMLPC	GGVGVDTDIT	WNEHSSNAA	RWAAGSVTDL	AFKVASRELK	NGFAVVRPPG	HHADHSTAMG	300									
301	FCFENSVAIA	CRQLQQQSKA	SKILIVDNDV	HHNGTQQT	YQDPSVLYIS	LHRHDDGNFF	PGSGAVDEVG	AGSGEGENVN	VAWAGGLDPP	MGDPEYLAAE	400									
401	RIVVMPIARE	FSPDLVLVSA	GFDAAEHHPA	PLGGYHVS	AK CFGYMTQQLM	NLAGGAVVLA	LEGGHDLTAI	CDASEACVAA	LLGNRVDPLS	EEGKQKPNL	500									
501	NSIRSLEAVI	RVHSKYWGCM	ORLASCPSW	VPRVPGADKE	EVEAVTALAS	LSVGILAE	DR PSEQLVEEEE	PMNL												
		10		20		30		40		50		60		70		80		90		100

Fig. 5B

	10	20	30	40	50	60	70	80	90	100
1	MFARSAGLCF	PWVPGVSHGG	DAEVLQAHP	TPTGRGAERR	PRPPDSSABG	DPGMLKPCGC	VPSQKVALK	VGAPFCTCGC	FQRFHLPKAC	PGQQGSPESA
101	RPRNRQPYAT	QNGPAPRPQV	LPGSSSRCCCH	GYICFLFDSS	QTAEVEVGWG	GDTGSQLRPL	LRGAVVNSRM	WDSQKEDSKP	DILRLQNTQL	FHSVSLSTDG
201	TQVSPGAHYC	SPITGAGCPRP	CADTFGPQPQ	PMDLRVGCORP	PVEPPPEPTL	LALQRPQRLH	HHLFLAGLQQ	QRSVEPMRVK	MELPACGATL	SLVPSLPAFS
301	IPRHQSQSST	PCPFLGCRPC	PQLSMDTPMP	ELQVGPQEQE	LRQLLHKDKS	KRSKEVATPA	QPSPTSQVPA	AACVACAVAS	SVVKQKLAEV	ILKKQQAALAE
401	RTVHPNSPGI	PYRSQGPCSG	QCPCSVPTPL	KQPMHSFCRT	LEPLETEGAT	RSMLSSEFLPP	VPSLPSDPPE	HFPLRKTVSE	PNLKLRYPK	KSLERRKNPL
501	LRKESAPPSL	RRRPAETLGD	SSPSSSSTPA	SGCSSPNDSE	HGPNPILGSE	ALLGQRLRLQ	ETSVAPFALP	TVSLLPAITL	GLPAPARADS	DRRTHPTLGP
601	RGPIILGSPHT	PLFLPHGLEP	EAGGTLPSRL	QPILLDDPSG	SHAPLLTVPG	LGPLPFHFAQ	SLMTTERLSG	SGLHWPLSRT	RSEPLPPSAT	APPPPGPMQP
701	RLEQLKTHVQ	VIKRSAPSE	KPRLRQIPSA	EDLETGCGP	GQVDDGLEH	RELGHGQPEA	RGAPAPLQHP	QVLLWEQRL	AGRLPRGSTG	DTVLLPLAQG
801	GHRPLSRAQS	SPAAPASLSA	PEPASQARVL	SSSETPARTL	PFTTGLIYDS	VMLKHQCCSG	DNSRHPEHAG	RIQSIWSRLQ	ERGLRSQCEC	LRGRKASLEE
901	LQSVHSERHV	LLYGTNPLSR	LKLDNGKLAG	LLAQRMFVML	PCGGVGPLAT	LSAFLASLAP	TVPQGLSRVS	WGLKPPPGPN	PKSRPAPCPW	GPGRGVGTTP
1001	LGPGSCVKPW	MMRALTLAPQ	VDITDTIWNEL	HSSNAARWAA	GSVTDLAFKV	ASRELKNGFA	VVRPPGHAD	HSTAMGFCFF	NSVAIACRQL	QQQSKASKIL
1101	IVDWDVHGN	GTQQTFYQDP	SVLYISLHRH	DDGNFFPGSG	AVDEVGAGSG	EGFNVNVAWA	GGILDPPMGDP	EYLAAFRIVV	MPIAREFSPD	LVLVSAGFDA
1201	AECHPAPLGG	YHVSAKCFGY	MTQQLMNLAG	GAUVLALEGG	HDLTAICDAS	EACVAALLGN	RVDPLSEEGW	KQKPNLNAIR	SLEAVIRVHS	KCGDGTALAE
1301	RLKDLGGTLP	HRGQILGFRG	QPGDLLLLWS	KTFVSDPGSN	GEHPPVRGYP	LSPPDGASRA	YQTVAPQGY	WGCMQRLASC	PDSWVPRVPG	ADKEEVEAVT
1401	ALASLSVGIL	AEDRPSEQLV	EEEEPMNL							

Fig. 6

cloned	1
deduced	1	MFARSAGLCFPWYPGYSHGGDAEEVLAQHPTPT
cloned	1
deduced	34	GRGAERRRPRPPDSSAEGDPQMLKPCGCPSPQK
cloned	1
deduced	67	YALKYGAPFCTCGCFQRFHLPKACPGQQGSPES
cloned	1
deduced	100	ARPRNRQPYATONGPAPRPQVLPGSSSRCCHGY
cloned	1
deduced	133	ICFLFDSSOTAEEYEGWGGDTGSOLRPLLRGAY
cloned	1
deduced	166	YNSRMWDSOKEDSKPDILRLQNTQLFHSYSLST
cloned	1
deduced	199	DGTOYSPGAHYCSPTGAGCPRPCADTPGPOPOP
cloned	1
deduced	232	MDLRVGQRPPVEPPPEPTLLALQRPQRLHHHLF
cloned	1
deduced	265	LAGLQQQRSYEPMARYKMELPACGATLSLYPSLP
cloned	1
deduced	298	AFSIPRHQSQSSTPCPFLGCRPCPQLSMDTPMP

Fig. 7

cloned	1
deduced	331	E L Q Y G P Q E Q E L R Q L L H K D K S K R S K E Y A T P A Q P S
cloned	1
deduced	364	P T S Q Y P A A A C Y A C A Y A S S Y Y K Q K L A E Y I L K K Q Q
cloned	1
deduced	397	A A L E R T Y H P N S P G I P Y R S Q G P C S G Q Q C P C S Y P T P
cloned	1
deduced	430	L K Q P W H S F C R T L E P L E T E G A T R S M L S S F L P P Y P
cloned	1
deduced	463	S L P S D P P E H F P L R K T Y S E P N L K L R Y K P K K S L E R
cloned	1
deduced	496	R K N P L L R K E S A P P S L R R R P A E T L G D S S P S S S S T
cloned	1
deduced	529	P A S G C S S P N D S E H G P N P I L G S E A L L G Q R L R L Q E
cloned	1
deduced	562	T S V A P F A L P T Y S L L P A I T L G L P A P A R A D S D R R T
cloned	1
deduced	595	H P T L G P R G P I L G S P H T P L F L P H G L E P E A G G T L P
cloned	1
deduced	628	S R L Q P I L L L D P S G S H A P L L T Y P G L G P L P F H F A Q

Fig. 7 (a)

cloned	1
deduced	661	SLMTTERLSGSGLHWPLSRTRSEPLPPSATAPP
cloned	1EQLKTHVOVIKRS AKPSEKPRLRQ
deduced	694	PPGPMQPRLEQLKTHVOVIKRS AKPSEKPRLRQ
cloned	25	IPSAEDLET DGGGGPGQVYDDGLEHRELGHGOPE
deduced	727	IPSAEDLET DGGGGPGQVYDDGLEHRELGHGOPE
cloned	58	ARGPAPLOQHPOYLLWEOQRLAGRLPRGSTGDT
deduced	760	ARGPAPLOQHPOYLLWEOQRLAGRLPRGSTGDT
cloned	91	YLLPLAOGGHRPLSRAOSSPAAPASLSAPEPAS
deduced	793	YLLPLAOGGHRPLSRAOSSPAAPASLSAPEPAS
cloned	124	QARYLSSSETPARTLPFTTGLIYDSYMLKHQCS
deduced	826	QARYLSSSETPARTLPFTTGLIYDSYMLKHQCS
cloned	137	CGDNSRHPEHAGRIOSIWSRLOERGLRSOCECL
deduced	859	CGDNSRHPEHAGRIOSIWSRLOERGLRSOCECL
cloned	190	RGRKASLEELQSYHSERHVLLYGTNPLSRLKLD
deduced	892	RGRKASLEELQSYHSERHVLLYGTNPLSRLKLD

Fig. 7 (b).

cloned	223	NGKLAGLLAQRMFYMLPCGGYG	-----
deduced	925	NGKLAGLLAQRMFYMLPCGGYG	PLATLSAFLAS
cloned	245	-----	-----
deduced	958	LAPTYPQGLSRYSWGLKPPPGPNPKSRPAPCPW	
cloned	245	-----	YDT
deduced	991	GPGRGYGTTPLGPGSCYKPWMMRALTLAPQ	YDT
cloned	248	DTIWNELHSSNAARWAAGSYTDLAFKYASRELK	
deduced	1024	DTIWNELHSSNAARWAAGSYTDLAFKYASRELK	
cloned	281	NGFAYYRPPPGHHADHSTAMGFCFFNSYAIACRQ	
deduced	1057	NGFAYYRPPPGHHADHSTAMGFCFFNSYAIACRQ	
cloned	314	LQQOSKASKILIDWDYHHGNGTQQTFFYQDPSY	
deduced	1090	LQQOSKASKILIDWDYHHGNGTQQTFFYQDPSY	
cloned	347	LYISLHRHDDGNFFPGSGAYDEVGAGSGEGFNY	
deduced	1123	LYISLHRHDDGNFFPGSGAYDEVGAGSGEGFNY	
cloned	380	NYAWAGGLDPPMGDPEYLAAFRIYMPIAREFS	
deduced	1156	NYAWAGGLDPPMGDPEYLAAFRIYMPIAREFS	

Fig. 7 (c)

cloned	413	PDLVLYSAGFDAAEGHPAPLGGYHYS AKCFGYM
deduced	1189	PDLVLYSAGFDAAEGHPAPLGGYHYS AKCFGYM
cloned	446	TOOLMNL AGGAYVLALEGGHDLTAICDASEACY
deduced	1222	TQOLMNL AGGAYVLALEGGHDLTAICDASEACY
cloned	479	AALLGNRYDPLSEEGWKOKPNLNSIRSLEAVIR
deduced	1255	AALLGNRYDPLSEEGWKOKPNLNAIRSLEAVIR
cloned	512	YHS
deduced	1288	YHS KCGDGT LAELRLKDLGGTLP HRGQILGFRC
cloned	515
deduced	1321	QPGDLLLYWSKIPYSDPGSNGEHPPYRGYPLSP
cloned	515 KYWGCMQRLASCPDSWYP
deduced	1354	PDGASRAYQTYAPOG KYWGCMQRLASCPDSWYP
cloned	533	RYPGADKEEVEAYTALASLSYGILAEDRPSEQL
deduced	1387	RYPGADKEEVEAYTALASLSYGILAEDRPSEQL
cloned	566	YEEEEPMNL
deduced	1420	YEEEEPMNL

Fig. 7 (d)

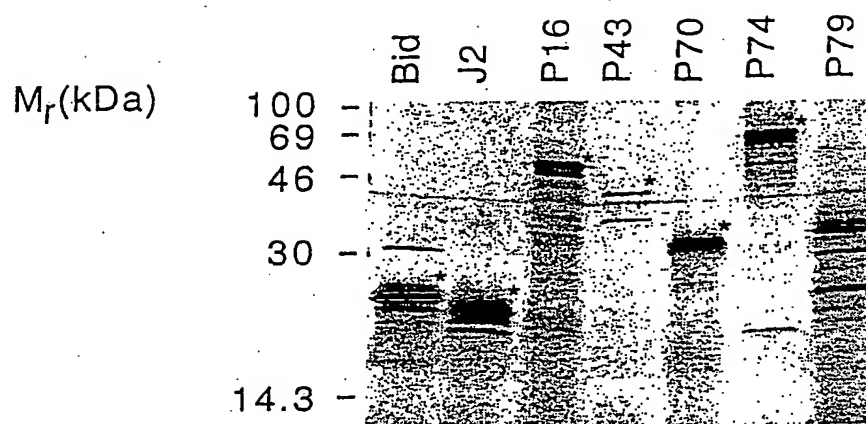
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 | : | | | | : : : | : | | : | | | : : | : : : : : : : :
 44 PSAVPMDLRLDHQFSLPVAEPALREQQLQQELLALKQKQKQIQRQILIAEF 93
 269 QQQORSV.....EPMRVKMELPACGATLSLVPSLPAFSIPRHQSQS 308
 | : | : : | : : : : | : : : : | : : : : | : : : :
 94 QRQHEQLSRQHEAQLHEHIKQQQEQMLAMKHQQELLEH..QRKLERHRREQ 141
 309 STPCPFLGCRPCPQLSMDTPMPELQVGPQEQELRQLLHKDKSKRSKEVAT 358
 | | : : | : | : | : | : | : | : | : | : | : | :
 142ELEKQHREQKLQQLKNKEKGKES..... 164
 359 PAQPSPTSQVPAAACVACAVASSVVKQKLAEVILKKQQAALERTVHPNSP 408
 | | | : | : | : | : | : | : | : | : | : | : | :
 165AVASTEVKMKLQEFVLNKKKALAHRL..... 191
 409 GIPYRSQGPCSGQCPCSVPTPLKQPWHSFCRTLEPLETEGATR.SMLSSF 457
 : | : : | : | : | : | : | : | : | :
 192NHCISSDPRYWYGKTQHSSLDQS 214
 458 LPPVPSLPS.....DPPEHFPLRKTVSEPNLKLRYKPK.KSLERR 496
 | | : : : | : | | | | : | | | | | : | | | |
 215 SPPQSGVSTSYNHPVLGMYDAKDDFPLRKTASEPNLKLRSRLKQKVAERR 264
 497 KNPLLRRKESAP..PSLRRRPAETLGDSSPSSSSTPASGCSSPND..... 539
 : : | | | : : : | : : : | : : : | : : : | : | : | : | :
 265 SSPLLRRKDGVPVVTALKKRPLDV...TDSACSSAPGSGPSSPNNSSGSVS 311
 540 .EHGPNPILGS...EALLGQRLRLQETSVAPFALPTVSLLPAILTLGLPA. 584
 | : | : | : | : | : | : | : | : | : | : | : | : | :
 312 AENGIAPAVPSIPAETSLAHLVAREGSAAPLPLYTSPSLPNITLGLPAT 361
 585PARADSDRRTHPTLGPRGPILGSPH.TPLFLPHGLEPEAGGTL 627
 : : | : : | : | : | : : : | : | : | : | : : : : :
 362 GPSAGTAGQQDTERLTLPALQQRSLFPGTHLTPYLSTSPLERDGGAAHS 411
 628 SRLQPIILLDPSGSHAPLLTVPGLGPLPFHFAQSLMTTERLSGS....GL 673
 | | : : | : : : | : | : | : | : | : | : | : | : | :
 412 PLLQHMVLLEQPPAQAPLVT..GLGALPLH.AQSLVGADRVSPSIHKLRQ 458
 674 HWPLSRTRSEPLPPSATAPPPPGPMQPRLEQLKTH.....VQVIKRS 715
 | | | : | : | : | : | : | : | : | : | : | : | : | :
 459 HRPLGRTQSAPLPQNAQALQHLVIQQQHQQFLEKHKQQFQQQQLQMNKII 508
 716 AKPSE.....KPRLRQIPSAEDLETGDDGGPG 741
 | | | | : | : | : : : : : : : : : : :
 509 PKPSEPARQPESHPEETEEELREHQALLDEPYLDRLPGQKEAHAQAG..V 556
 742 QVVDDGLEHRELGHGQPEARGP...APLQQHP.....QVLLWEQQR 779
 | | : : | : | : | : | : | : | : | : | : | : | : | :
 557 QVKQEPIDESDE.....EEAEPPREVEPGRQPSQELLFRQQALLLEQQR 601
 780 LAGRLPRGSTGDTVLLPLAQGGHRPLSRAQSSPA.APASLSAPEPASQAR 828
 : : : : : : : | | | | | | | | | | : : | : | : : |
 602 IHQLRNYQASMEAAGIPVSFGGHRPLSRAQSSPASATFPVSVQEPPTKPR 651
 829 VLSSSETPARTLPFTTGLIYDSVMLKHQCSCGDNRRHPEHAGRIQSIWSR 878
 | | | | : | : : | | | | : | : : | | | | | | | | | |
 652FTTGLVYDTLMLKHQCTCGSSSSHPEHAGRIQSIWSR 688

Fig. 8

Fig. 8 (a)

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A



B

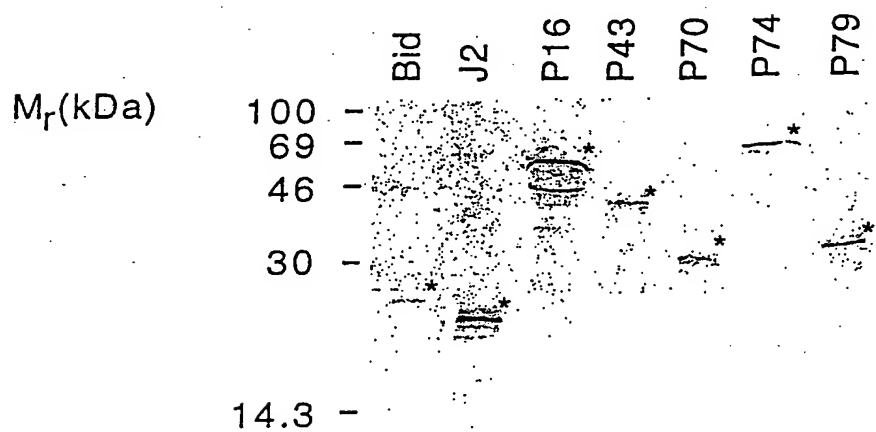


Fig. 9

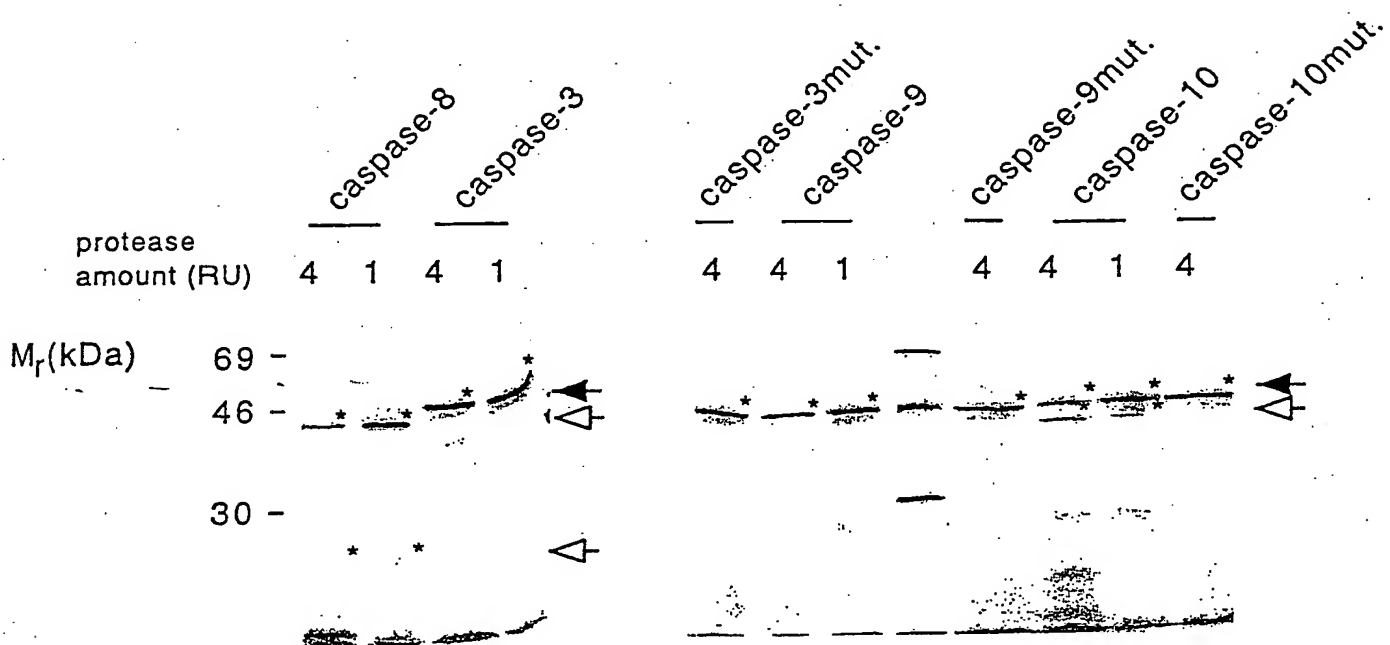


Fig. 10

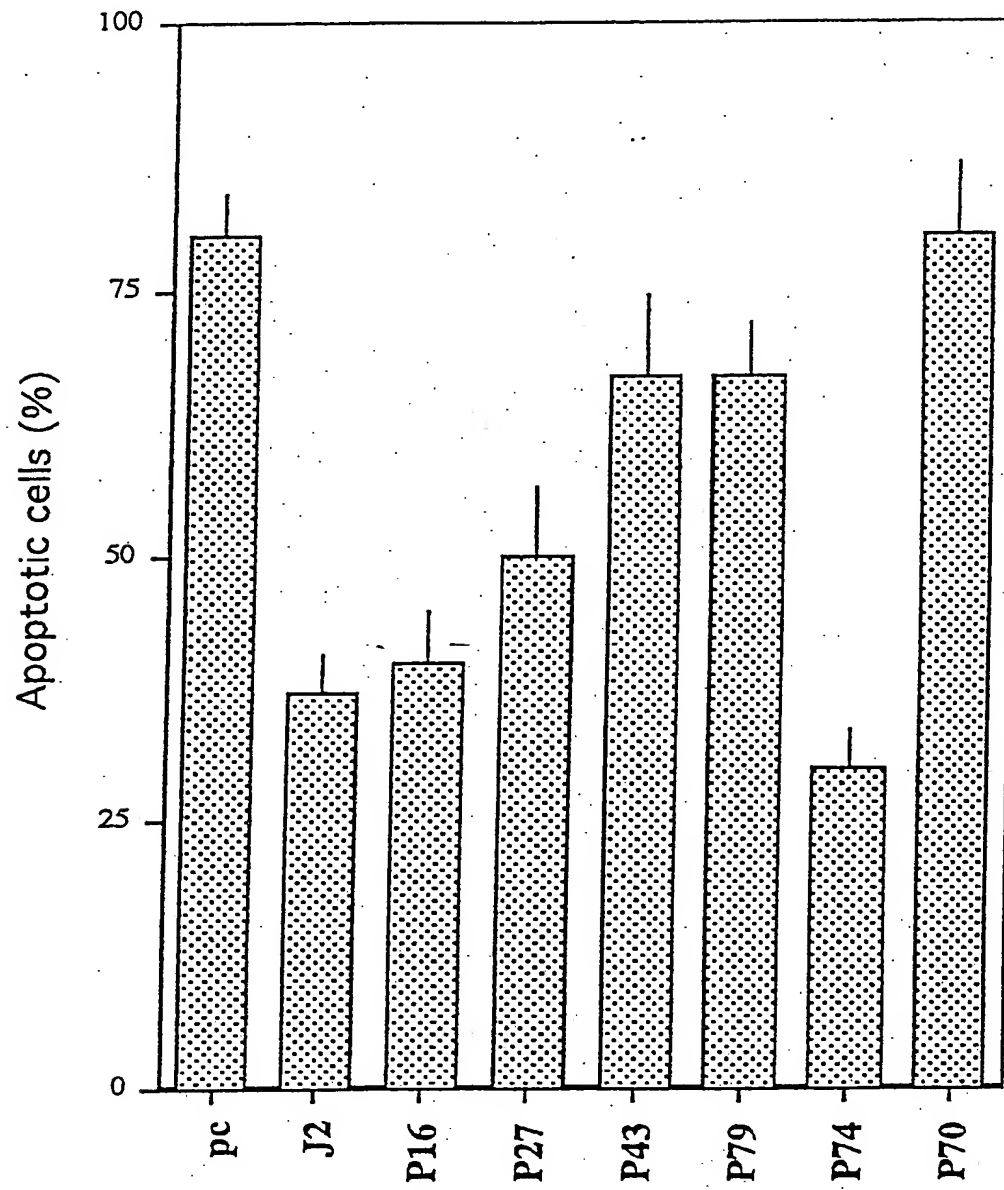


Fig. 11

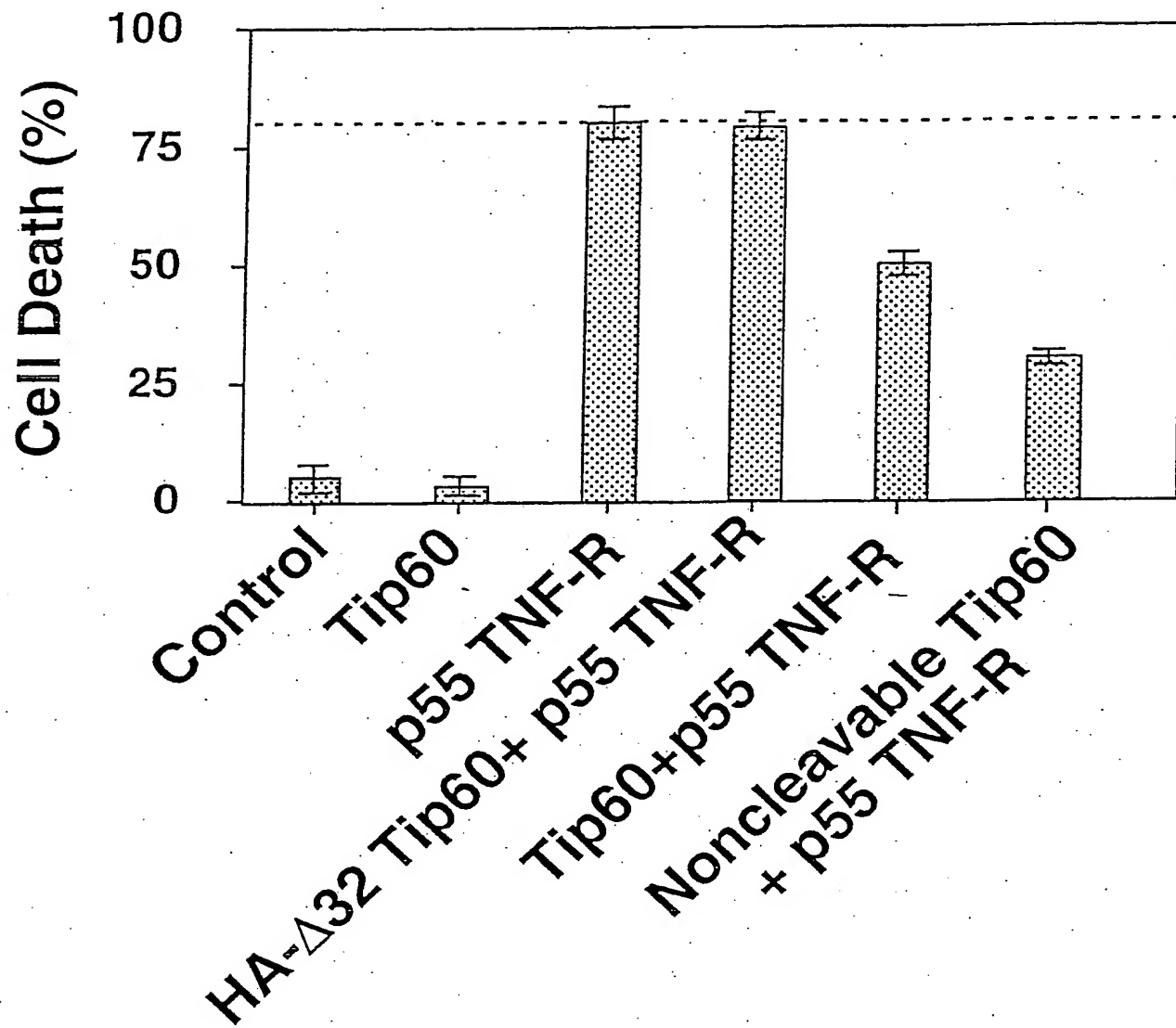


Fig. 12